Online-Only Abstracts

Predictors of clinical and microbiological treatment failure in patients with methicillin-resistant *Staphylococcus aureus* (MRSA) bacteraemia: a retrospective cohort study in a region with low MRSA prevalence

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Original Submission: 26 October 2012; **Revised Submission:** 11 December 2012; **Accepted:** 15 January 2013
Editor: G. Lina
Article published online: 11 February 2013
Clin Microbiol Infect 2013; **19:** E291–E297
10.1111/1469-0691.12169

Abstract

Invasive infections with methicillin-resistant *Staphylococcus aureus* (MRSA) have been associated with increased morbidity and mortality. The aim of the present study was to identify independent predictors of early mortality and treatment failure in patients with MRSA bacteraemia. A total of 132 adult patients who developed MRSA bacteraemia during hospitalization in the University Hospital of Vienna between 2000 and 2011 were screened and 124 were included in a retrospective cohort study. Patient demographics, source of bacteraemia, antimicrobial treatment and microbiological characteristics were evaluated. The 28-day crude mortality was 30.6%. Predictors of early mortality identified in multivariate Cox regression analysis included higher patient age (adjusted hazard ratio (aHR) 1.03, 95% CI 1.01–1.06, p 0.006), pneumonia (aHR 3.86, 95% CI 1.83–8.12, p <0.001) and failure to use MRSA active treatment (aHR 8.77, 95% CI 3.50–21.93, p <0.001). Ninety-one (73.4%) patients received glycopeptides as specific MRSA treatment. Of 63 patients treated with vancomycin, only 14 (22.6%) patients had aimed trough levels of 15–20 mg/L. Vancomycin MIC ≥2 mg/L was detected in 28.2% and was associated with glycopeptide pretreatment (p 0.001). All MRSA isolates were susceptible to linezolid and tigecycline. Persistent bacteraemia ≥7 days was documented in 25 (20.2%) patients. Independent determinants for microbiological eradication failure in patients with MRSA bacteraemia included endocarditis (p <0.001) and vancomycin trough levels (p 0.014), but not vancomycin MIC. Failure of clinical and microbiological eradication of MRSA among patients with MRSA bacteraemia was associated with clinical entity rather than with bacterial traits. Pharmacokinetic parameters seem to be decisive on microbiological and clinical success.

Streptococcus pneumoniae ocular infections, prominent role of unencapsulated isolates in conjunctivitis

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Original Submission: 31 August 2012; **Revised Submission:** 31 January 2013; **Accepted:** 11 February 2013
Editor: J.-L. Mainardi
Article published online: 20 March 2013
Clin Microbiol Infect 2013; **19:** E298–E305
10.1111/1469-0691.12196

Abstract

The aim of this study was to determine the characteristics and shifts in serotype distribution of pneumococcal isolates causing ocular infections in a region of northern Spain in two periods: 1999–2010 for episodes of conjunctivitis (n = 612) and 1980–2010 for uncommon and more severe non-conjunctival ocular infections (n = 36). All isolates were serotyped and non-typeable isolates were confirmed as unencapsulated by multiplex-PCR of the *lytA*, *ply* and *cpsA* genes. Genotyping was done by pulsed-field gel electrophoresis and multi-locus sequence typing. Most conjunctivitis cases occurred in children under 5 years old (89.5%), and more severe non-conjunctival ocular infections occurred in patients older than 25 years (86.1%). Unencapsulated isolates were detected in 213 conjunctivitis episodes (34.8%) and one non-conjunctival infection (2.8%). Rates of unencapsulated isolates were similar throughout the study. Among 399 conjunctival encapsulated isolates, the most prevalent were serotypes 19A (n = 53), 15B (n = 30), 6A (n = 27), 19F (n = 25), 23F (n = 21) and 6B (n = 17). The most prevalent serotypes in non-conjunctival infections were serotype 3 (n = 4), 23F (n = 4), 6B (n = 3) and 19A (n = 3). Conjunctivitis caused by serotypes included in the hepta-valent pneumococcal conjugate vaccine steadily decreased, accounting for 34.9% (22/63) in 1999–2001, 19.7% (23/117) in 2002–04, 13.6% (33/242) in 2005–07 and 3.2% (6/190) in 2008–10. Among the 213 unencapsulated isolates, 31 different pulsed-field gel electrophoresis patterns were identified. The main clonal complexes (CC) were CC941 (ST941, ST942), CC448 (ST448) and CC344 (ST344, ST3097). CC941 was the predominant CC in 1999–2001, 2002–04 and 2005–07, being replaced by CC448 in 2008–10. The multidrug-resistant CC344 was present throughout the study.